In the Specification:

Please amend the specification as indicated below.

Please replace the paragraph beginning on page 5, line 26, with the following rewritten paragraph:

The term "**STR50**", as used herein, also known as "MEG-3", refers to the expressed polypeptide of either variant of the novel gene STR50, derived from any organism, preferably man, and splice variants thereof. In addition, this term is understood to encompass polypeptides resulting from minor alterations in the coding sequence of either variant of the STR50 gene, such as, *inter alia*, point mutations, substitutions, deletions and insertions which may cause a difference in a few amino acids between the resultant polypeptide and the naturally occurring STR50 polypeptides. Polypeptides encoded by nucleic acid sequences which bind to the STR50 coding sequences or genomic sequence under conditions of highly stringent hybridization, which are well-known in the art (for example Ausubel et al., Current Protocols in Molecular Biology, John Wiley and Sons, Baltimore, Maryland (1988), updated in 1995 and 1998), are also encompassed by this term. Chemically modified STR50 polypeptides or chemically modified fragments of the STR50 polypeptide are also included in the term, so long as the biological activity is retained. The cDNA sequence (including untranslated regions) and amino acid sequence of the long variant of STR50 are set out in Figures ~~1~~ 1A-1C (SEQ ID NO:1) and 2 (SEQ ID NO:2) respectively; The cDNA sequence (including untranslated regions) and amino acid sequence of the short variant of STR50 are set out in Figures 3A-3C (SEQ ID NO:3) and 4 (SEQ ID NO:4) respectively. Additionally, molecules comprising the N-terminus of the polypeptides encoded by the sequences set forth in Figure 2 (SEQ ID NO:2)

and Figure 4 (SEQ ID NO:4) are also encompassed by this term, so long as they retain STR50 biological activity. The "N-terminus" as used herein typically refers to 10 consecutive amino acids starting from position 1 of the amino acid sequence (i.e., SEQ ID NO:2 or SEQ ID NO:4).

Please replace the paragraph beginning on page 8, line 17, with the following rewritten paragraph:

The present invention further provides a purified polypeptide encoded by a polynucleotide having at least 15, optionally at least 30, 50, 70 or even 100 consecutive nucleotides from position 1 to position 922 of the sequence depicted in Figures ~~1~~ 1A-1C. In addition, the present invention provides a purified polypeptide encoded by a polynucleotide having at least 15, optionally at least 30, 50, 70 or even 100 consecutive nucleotides from position 1 to position 766 of the sequence depicted in Figures ~~3~~ 3A-3C.

Please replace the paragraph beginning on page 8, line 23, with the following rewritten paragraph:

Any purified polypeptides encoded by polynucleotides of at least 15 consecutive nucleotides depicted in either Figures ~~1~~ 1A-1C or Figures ~~3~~ 3A-3C are considered to be a part of the present invention, provided that they are not disclosed in Genbank ID number gi: 14248494; these polynucleotides are also considered a part of the present invention.

Please replace the paragraph beginning on page 11, line 7, with the following rewritten paragraph:

Further in this aspect, the invention provides a purified polynucleotide which encodes a polypeptide having the

sequence set forth in SEQ ID NO:2, and a purified polynucleotide which encodes a polypeptide having the sequence set forth in SEQ ID NO:4. In addition, a polynucleotide having between 10 and 922 consecutive nucleotides from position 1 to position 922 of SEQ ID NO:1, and a polynucleotide having between 10 and 766 consecutive nucleotides from position 1 to position 766 of SEQ ID NO:3 are also provided. Any polynucleotide comprising at least 15 consecutive nucleotides from the sequence depicted in Figures ~~1~~ 1A-1C or from the sequence depicted in Figures ~~3~~ 3A-3C is also considered a part of the present invention, provided that it is not disclosed in Genbank ID number gi: 14248494.

Please replace the paragraph beginning on page 12, line 5, with the following rewritten paragraph:

The AS fragment of the present invention preferably has the sequence depicted in Figures ~~3~~ 3A-3C or a homologous sequence thereof. Particular AS fragments are the AS of the DNA encoding the particular fragments of STR50 described above. For delivery of AS fragments see Example 10.

Please replace the paragraph beginning on page 12, line 30, with the following rewritten paragraph:

By "STR50 gene" is meant the STR50 coding sequence open reading frame, as shown in Figures ~~1~~ 1A-1C (SEQ ID NO:1), or any sequences derived from the sequence of Figures ~~1~~ 1A-1C which have undergone mutations, such as substitutions, deletions and insertions, as described herein, and any nucleic acid that encodes the STR50 polypeptide, as defined herein.

Please replace the paragraph beginning on page 19, line 10, with the following rewritten paragraph:

The expression level of the polypeptide can be assessed by assaying for mRNA encoding the polypeptide (such as that described in Figures ~~1~~ 1A-1C or Figures ~~3~~ 3A-3C, or a fragment or homolog thereof), or by method of an immunoassay using antibodies which detect the polypeptide. Both detection of mRNA and immunoassays can be performed by methods well known in the art (see Examples 2-5 for further details). Measurement of level of the STR50 polypeptide is determined by a method selected from the group consisting of immunohistochemistry (Microscopy, Immunohistochemistry and Antigen Retrieval Methods: For Light and Electron Microscopy, M.A. Hayat (Author), Kluwer Academic Publishers, 2002; Brown C.: "Antigen retrieval methods for immunohistochemistry", *Toxicol Pathol* 1998; 26(6): 830-1), western blotting (Laemmeli UK: "Cleavage of structural proteins during the assembley of the head of a bacteriophage T4", *Nature* 1970;227: 680-685; Egger & Bienz, "Protein (western) blotting", *Mol Biotechnol* 1994; 1(3): 289-305), ELISA (Onorato et al., "Immunohistochemical and ELISA assays for biomarkers of oxidative stress in aging and disease", *Ann NY Acad Sci* 1998 20; 854: 277-90), antibody microarray hybridization (Huang, "detection of multiple proteins in an antibody-based protein microarray system, *Immunol Methods* 2001 1; 255 (1-2): 1-13) and targeted molecular imaging (Thomas, Targeted Molecular Imaging in Oncology, Kim et al (Eds)., Springer Verlag, 2001).

Please replace page 29 with the following:

BRIEF DESCRIPTION OF THE FIGURES

Figures ~~1~~ 1A-1C depicts the nucleic acid sequence of the long splice variant of human STR50 (SEQ ID NO:1).

Figure 2 depicts the amino acid sequence of the long splice variant of human STR50 (SEQ ID NO:2).

Figures ~~3~~ 3A-3C depicts the nucleic acid sequence of the short splice variant of human STR50 (SEQ ID NO:3).

Figure 4 depicts the amino acid sequence of the short splice variant of human STR50 (SEQ ID NO:4).

Please replace the paragraph beginning on page 43, line 25, with the following rewritten paragraph:

Figures ~~1~~ 1A-1C represents the long variant, which contains an additional exon; this variant is 4008bp long, with a 2463bp long ORF which translates into a 821 amino acid long polypeptide.

Figures ~~3~~ 3A-3C represents the short variant which is 4533bp long with 2373bp ORF which translates into a 791 amino acid long polypeptide.